Amendments to the Specification:

In the specification:

Insert the following paragraph at page 1, immediately below the title of the application:

CROSS REFERENCE TO RELATED APPLICATIONS

--This application is a continuation (and claims the benefit of priority under 35 USC 120) of U.S. application serial no. 09/848,838, filed May 3, 2001, which claims priority to, and is a divisional of, U.S. application serial No. 09/433,598, filed November 2, 1999, which claims priority under 35 U.S.C. Section 119(e) to provisional patent application 60/107,268 filed on November 4, 1998. The disclosure of the prior application is considered part of (and is incorporated by reference in) the disclosure of this application.--

Replace the paragraph beginning at page 5, line 13, with the following rewritten paragraph:

--**Fig. 1** shows the nucleotide sequence analysis of *Hp fucT2*. (A) Gene organization of *Hp fucT2* region in the genome of *H. pylori* 26695 and UA802. GW44 and GW32 indicate the two primers used for cloning *Hp fucT2* genes. (B) Nucleotide sequences of the center region of *Hp fucT2* showing the features (simple repeats) responsible for frameshift between prototype (UA802; SEQ ID NO:7) and variant type (26695; SEQ ID NO:6) genes. The divergent nucleotides between the two sequences are marked by "x". Due to the different repeat number of poly C residues, the initiating reading frame of 26695 *fucT2* (HP0094) encounters a TGA stop codon (marked with asterisks) shortly after the poly-C region. About 110 bp further downstream, there appears a potential start codon ATG (marked with dots) in the -1 frame (HP0093), which is the same as the reading frame of 802 *fucT2*. The three putative X XXY YYZ motifs (X, Y, and Z represent specific nucleotides in a particular reading from) are given in bold face and underlined. Additional elements for programmed translation frameshift in 26695 *fucT2* resembling those in *E. coli dnaX* gene are also underlined. (C) The putative 26695 *fucT2* translation frameshift cassette. Shown is the mRNA structure (SEQ ID NO:8) deduced from the DNA sequence in line

2 of (B). The AAAAAAG heptamer (bold) is a highly slippery sequence identified in other DNA sequences. UGA (sidelined in the stem structure) is the stop codon in the initiating frame (0 frame). SD indicates an internal Shine-Dalgarno-like sequence. According to the *E. coli dnaX* frameshift model, AAAAAAG sequence is the frameshift site, and both upstream SD sequence and downstream stem-loop structure enhance frameshifting. (D) Shows the amino acid sequence and nucleic acid sequence for α1,2 fucosyltransferase (SEQ ID NOs:2 and 1, respectively).--

Replace the paragraph beginning at page 6, line 7, with the following rewritten paragraph:

--**Fig. 2** shows an analysis of the deduced Amino acid (aa) sequence of *Hp fucT2* . (A) Schematic representation of the domain structures of mammalian and bacterial α(1,2) fucosyltransferases. Cyt, cytoplasmic. TM, transmembrane. Hatched boxes represent three highly conserved aa sequence motifs. (B) Alignment of the three motifs of aa sequences which are highly conserved in all prokaryotic and eukaryotic α(1,2) fucosyltransferases (Motif I sequences from top to bottom are SEQ ID NOs:9 to 13, respectively; Motif II sequences from top to bottom are SEQ ID NOs:14 to 18, respectively; and Motif III sequences from top to bottom are SEQ ID NOs:19 to 23, respectively). The length (in aa) of each protein is given in parentheses after the name of organisms, and the positions of each motif within the protein are labeled in parentheses after each amino acid sequence. Ye, Y. enterocolitica. Ll, Lactococcus lactis. Accession numbers of these sequences are: M35531 (man FUT1), U17894 (man FUT2), AF076779 (Hp FucT2, from the prototype fucT2 of UA802), U46859 (Ye WbsH), and U93364 (Ll EpsH).--

Insert the paper copy of the Sequence Listing following the Abstract.